



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

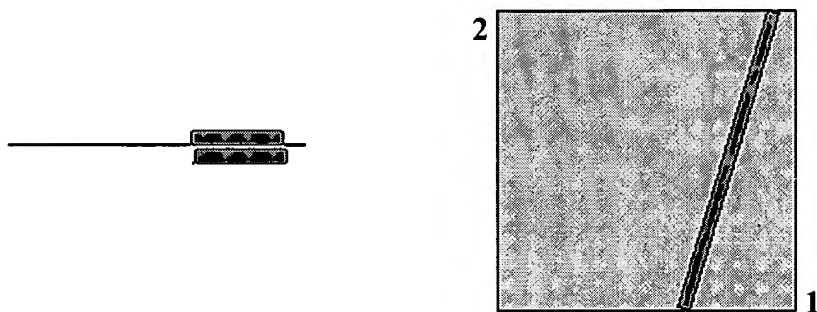
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒

Sequence 1 [gi_40381](#) Clostridium botulinum botA gene for type A neurotoxin **Length** 4292 (1 .. 4292)

Sequence 2 [lcl|seq_2](#)

Length 1323 (1 .. 1323)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 412 bits (214), Expect = e-111

Identities = 937/1302 (71%)

Strand = Plus / Plus

```
Query: 2666 tctacatttactgaatatattaagaatattattaatacttctatattgaatttaagatat 2725
          ||||| || ||||| || || ||||| || || ||||| || || ||||| || || |||||
Sbjct: 16   tctaccttcaactgaatacatcaagaacatcatcaatacctccatcctgaacctgcgctac 75
```

```
Query: 2726 gaaagtaatcatttaatagacttatctaggtatgcatcaaaaataaatattggtagtaaa 2785
          ||| ||||| | || ||||| || || ||||| || || ||||| || || |||||
Sbjct: 76   gaatccaatcacctgatcgacctgtctcgctacgcttccaaaatcaacatcggttctaaa 135
```

```
Query: 2786 gtaaattttgatccaatagataaaaaatcaaattcaattatttaatttagaaagtagtaaa 2845
          || || || ||||| || || ||||| || || ||||| || || ||||| || || |||||
Sbjct: 136  gttaacttcgatccgatcgacaagaatcagatccagctgttcaatctggaatcttccaaa 195
```

```
Query: 2846 attgaggtaatttttaaaaaatgctattgtatataatagtatgtatgaaaatttttagtact 2905
          || || || || || || ||||| ||||| || ||||| ||||| || || |||||
Sbjct: 196  atcgaagttatcctgaagaatgctatcgatatacaactctatgtacgaaaacttctccacc 255
```


X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)